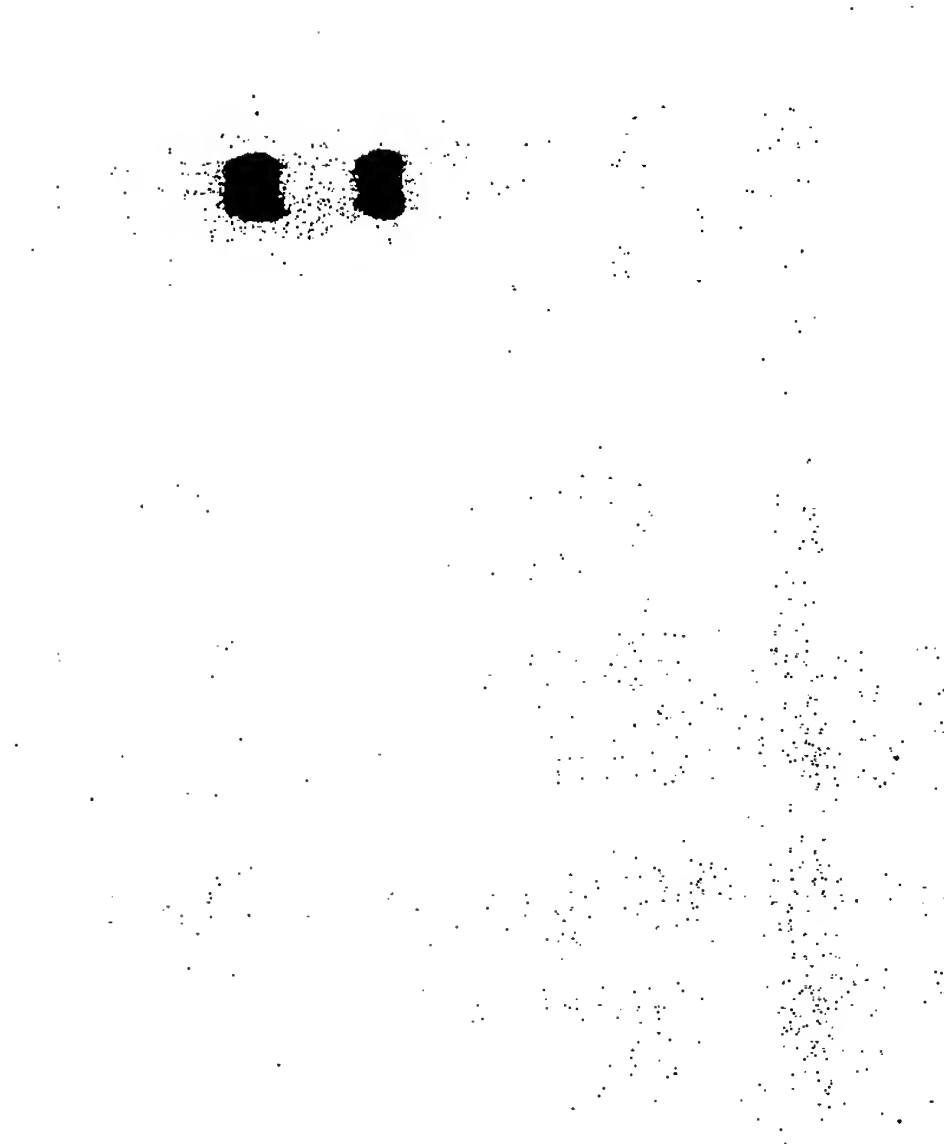


1/3



ovary
liver
muscle
testis
spleen
intestine
pancreas
seminal vesicle
kidney
brain
thymus
lung
heart

FIG. 1

2 / 3

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1  CGGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGAC 60
   R A R R R T P T C E P A T P L C C R R D
61 CATTACGTAGACTTCCAGGAAGTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTAC 120
   H Y V D F Q E L G W R D W I L Q P E G Y
121 CAGCTGAATTACTGCAGTGGGCAGTGGCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCT 180
   Q L N Y C S G Q C P P H L A G S P G I A
181 GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTGGCCTGCCAGT 240
   A S F H S A V F S L L K A N N P W P A S
241 ACCTCCTGTGTGTCTCCCTACTGCCCGAAGGCCCTCTCTCTCTCTACCTGGATCATAAT 300
   T S C C V P T A R R P L S L L Y L D H N
301 GGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 360
   G N V V K T D V P D M V V E A C G C S *
  
```

FIG. 2

<u>Family member</u>	<u>% identity with GDF-12</u>
GDF-1	43
GDF-3	36
GDF-5	36
GDF-6	39
GDF-7	42
GDF-9	30
BMP-3	37
BMP-2	43
BMP-4	42
Vgr-1	41
OP-1	40
BMP-5	38
OP-2	39
MIS	30
Inhibin- α	27
Inhibin-BA	47
Inhibin-BB	50
Nodal	38
GDNF	21
TGF- β 1	36
TGF- β 2	36
TGF- β 3	41

FIG. 4

1 GAGCTGTGAGGGTCAAGCACAGCTATCCATCAGATGATCTACTTTTCAGCCTTCCTGAGTC 60 3/3
61 CCAGACAATAGAAGACAGGTGGCTGTACCCTTGGCCAAGGGTAGGTGTGGCAGTGGTGTGTC 120
121 TGCTGTCACTGTGCCCCTCATTGGCCCCCAGCAATCAGACTCAACAGACGGAGCAACTGCC 180
181 ATCCGAGGCTCCTGAACCAGGGCCATTACACCAGGAGCATGCGGCTCCCTGATGTCCAGCT 240
M R L P D V Q L
241 CTGGCTGGTGTGCTGTGTGGGCACTGGTGGGAGCACAGGGGACAGGGTCTGTGTGTCCCTC 300
W L V L L W A L V R A Q G T G S V C P S
301 CTGTGGGGGCTCCAAACTGGCACCCCAAGCAGAACGAGCTCTGGTGTGCTGGAGCTAGCCAA 360
C G G S K L A P Q A E R A L V L E L A K
361 GCAGCAAATCCTGGATGGGTGTCACCTGACCAGTCGTCCAGAATAACTCATCCTCCACC 420
Q Q I L D G L H L T S R P R I T H P P P
421 CCAGGCAGCGCTGACCAGAGCCCTCCGGAGACTACAGCCAGGGAGTGTGGCTCCAGGGAA 480
Q A A L T R A L R R L Q P G S V A P G N
481 TGGGGAGGAGGTCATCAGCTTTGCTACTGTACAGACTCCACTTCAGCCTACAGCTCCCT 540
G E E V I S F A T V T D S T S A Y S S L
541 GCTCACTTTTTCACCTGTCCACTCCTCGGTCCCACCACCTGTACCATGCCCGCCTGTGGCT 600
L T F H L S T P R S H H L Y H A R L W L
601 GCACGTGCTCCCCACCCTTCCTGGCACTCTTTGCTTGAGGATCTTCCGATGGGGACCAAG 660
H V L P T L P G T L C L R I F R W G P R
661 GAGGAGGCGCCAAGGGTCCCGCACTCTCCTGGCTGAGCACCACATCACCAACCTGGGCTG 720
R R R Q G S R T L L A E H H I T N L G W
721 GCATACCTTAACCTCTGCCCTCTAGTGGCTTGAGGGGTGAGAAGTCTGGTGTCTGAAACT 780
H T L T L P S S G L R G E K S G V L K L
781 GCAAETAGACTGCAGACCCCTAGAAGGCAACAGCACAGTTACTGGACAACCGAGGCGGCT 840
Q L D C R P L E G **N S T** V T G Q P R R L
841 CTTGGACACAGCAGGACACCAGCAGCCCTTCCTAGAGCTTAAGATCCGAGCCAATGAGCC 900
L D T A G H Q Q P F L E L K I R A N E P
901 TGGAGCAGGCGGGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGCGACCCCTTATGTTG 960
G A G **R A R R R** T P T C E P A T P L C C
961 CAGGCGAGACCATTACGTAGACTTCCAGGAAGTGGGATGGCGGGACTGGATACTGCAGCC 1020
R R D H Y V D F Q E L G W R D W I L Q P
1021 CGAGGGGTACCAGCTGAATTACTGCAGTGGGCACTGCCCTCCCCACCTGGCTGGCAGCCC 1080
E G Y Q L N Y C S G Q C P P H L A G S P
1081 AGGCATTGCTGCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTG 1140
G I A A S F H S A V F S L L K A N N P W
1141 GCCTGCCAGTACCTCCTGTTGTGTCCCTACTGCCCCAAGGCCCCCTCTCTCTCTACCT 1200
P A S T S C C V P T A R R P L S L L Y L
1201 GGATCATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGG 1260
D H N G N V V K T D V P D M V V E A C G
1261 CTGCAGCTAGCAAGAGGACCTGGGGCTTTGGAGTGAAGAGACCAAGATGAAGTTTCCCAG 1320
C S *
1321 GCACAGGGCATCTGTGACTGGAGGCATCAGATTCCTGATCCACACCCCAACCCAACAACC 1380
1381 ACCTGGCAATATGACTCACTTGACCCCTATGGGACCCAAATGGGCACTTTCTTGTCTGAG 1440
1441 ACTCTGGCTTATTCCAGGTTGGCTGATGTGTTGGGAGATGGGTAAAGCGTTTCTTCTAAA 1500
1501 GGGGTCTACCCAGAAAGCATGATTTCTGCCCCAAGTCCTGTGAGAAGATGTCAGGGACT 1560
1561 AGGGAGGGAGGGAGGGAAGGCAGAGAAAAATTACTTAGCCTCTCCCAAGATGAGAAAGTC 1620
1621 CTCAAGTGAGGGGAGGAGGAAGCAGATAGATGGTCCAGCAGGCTTGAAGCAGGGTAAGCA 1680
1681 GGCTGGCCCAGGGTAAGGGCTGTTGAGGTACCTTAAGGGAAGGTCAAGAGGGAGATGGGC 1740
1741 AAGGCGCTGAGGGAGGATGCTTAGGGGACCCCCAGAAACAGGAGTCAGGAAAATGAGGCA 1800
1801 CTAAGCCTAAGAAGTTCCCTGGTTTTTCCCAGGGGACAGGACCCACTGGGAGACAAGCAT 1860
1861 TTATACTTTCTTTCTTTCTTTTATTTTTTTGAGATCGAGTCTCGCTCTGTCACCAGGCT 1920
1921 GGAGTGCAGTGACACGATCTTGGCTCACTGCAACCTCCGTCTCCTGGGTTCAAGTGATTC 1980
1981 TTCTGCCTCAGCCTCCCCGAGCAGCTGGGATTACAGGCGCCCACTAATTTTTGTATTCTTA 2040
2041 GTAGAAACGAGGTTTCAACATGTTGGCCAGGATGGTCTCAATCTCTTGACCTCTTGATCC 2100
2101 ACCCGACTTGGCCTCCCGAAGTGATGAGATTATAGGCGTGAGCCACCGCGCCTGGCTTAT 2160
2161 ACTTTCTTAATAAAAAGGAGAAAGAAAATCAACAAATGTGAGTCATAAAGAAGGGTTAGG 2220
2221 GTGATGGTCCAGAGCAACAGTTCTTCAAGTGTAATCTGTAGGCTTCTGGGAGGTCCCTTT 2280
2281 TCAGGGGTGTCCACAAAGTCAAAGCTATTTTCATAATAATACTAACATGTTATTTGCCTT 2340
2341 TTGAATTCTCATTATCTTAAATTTGTATTGTGGAGTTTTCCAGAGGCCGTGTGACATGTG 2400
2401 ATTACATCATCTTTCTGAC 2419

FIG. 3